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#### SUPPLEMENTARY MATERIAL

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# Overexpression of MYBL2 predicts poor prognosis and promotes oncogenesis in endometrial carcinoma

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**Table S1**. 10 DEGs copy number p-value data.

Gene	Spearman	p	Pearson	p
MYBL2	0.34	4.08E-15	0.54	1.43E-39
CCNB2	0.13	4.72E-03	0.11	0.01
ZNF695	0.26	1.99E-09	0.29	2.89E-11
TCF23	0.01	0.92	-0.06	0.42
ASPA	-0.02	0.64	-0.03	0.44
TROAP	0.22	5.21E-07	0.24	2.78E-08
CLEC4M	-0.08	0.29	0.03	0.68
CDC25C	0.01	0.86	0.15	6.17E-04
SKA3	0.07	0.12	0.20	8.45E-06
FGF10	-0.03	0.73	-0.03	0.67

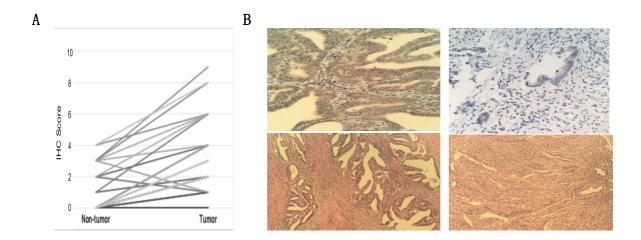
Download the copy number of 10 DEGs, compare the Spearman and Pearson of each gene, and the p-value for each gene. The p-value of *MYBL2* is the lowest, so the CNAs of *MYBL2* gene is the most obvious.

Table S2. 5 DEGs Survival analysis.

	p-valu		
Gene	0S	DFS	
ASPS	0.46	0.172	
MYBL2	0.020	0.014	
TROAP	0.685	0.255	
CCNB2	0.030	0.856	
CDC25C	0.416	0.295	

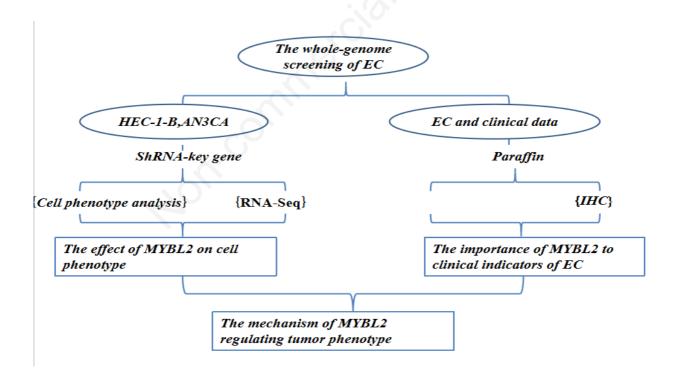
The five most significant genes in EC were verified by GEO data set. Both overall survival (OS) and disease-free survival (DFS) of MYBL2 gene are meaningful (p<0.05).





#### Figure S1.

**IHC of** *MYBL2* **expression in EC tissue**. A) the IHC scores of EC and adjacent tissues. B) IHC and HE staining results of EC and adjacent tissues. In IHC, *MYBL2* stained positively in the nucleus and cytoplasm.



### Figure S2.

Flow chart of the study.

